

## SEQUENCE LISTING

&lt;110&gt; WILEY, Steven R.

&lt;120&gt; TWEAK Receptor

&lt;130&gt; 2968-B

&lt;140&gt; to be assigned

&lt;141&gt; 2000-12-19

&lt;150&gt; 60/172,878

&lt;151&gt; 1999-12-20

&lt;150&gt; 60/203,347

&lt;151&gt; 2000-05-10

&lt;160&gt; 7

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (52)..(873)

&lt;220&gt;

<223> Description of Artificial Sequence: human TWEAK  
fusion protein construct

&lt;400&gt; 1

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tctcgagggc cacgcgttta aacgtcgagg tacctatccc gggccgccac c atg gct 57
                                     Met Ala
                                     1

aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc ctg ctc tgc ctg 105
Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
      5                      10                      15

ccc tgg ctt caa gag ggc agt gca act agt tct gac cgt atg aaa cag 153
Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met Lys Gln
      20                      25                      30

ata gag gat aag atc gaa gag atc cta agt aag att tat cat ata gag 201
Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu
      35                      40                      45                      50

aat gaa atc gcc cgt atc aaa aag ctg att ggc gag cgg act aga tct 249
Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Arg Ser
      55                      60                      65

agt ttg ggg agc cgg gca tcg ctg tcc gcc cag gag cct gcc cag gag 297
Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu
      70                      75                      80

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gag ctg gtg gca gag gag gac cag gac ccg tcg gaa ctg aat ccc cag 345  
 Glu Leu Val Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln  
 85 90 95

aca gaa gaa agc cag gat cct gcg cct ttc ctg aac cga cta gtt cgg 393  
 Thr Glu Glu Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg  
 100 105 110

cct cgc aga agt gca cct aaa ggc cgg aaa aca cgg gct cga aga gcg 441  
 Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala  
 115 120 125 130

atc gca gcc cat tat gaa gtt cat cca cga cct gga cag gac gga gcg 489  
 Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp Gly Ala  
 135 140 145

cag gca ggt gtg gac ggg aca gtg agt ggc tgg gag gaa gcc aga atc 537  
 Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala Arg Ile  
 150 155 160

aac agc tcc agc cct ctg cgc tac aac cgc cag atc ggg gag ttt ata 585  
 Asn Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile  
 165 170 175

gtc acc cgg gct ggc ctc tac tac ctg tac tgt cag gtg cac ttt gat 633  
 Val Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp  
 180 185 190

gag ggg aag gct gtc tac ctg aag ctg gac ttg ctg gtg gat ggt gtg 681  
 Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val  
 195 200 205 210

ctg gcc ctg cgc tgc ctg gag gaa ttc tca gcc act gcg gcc agt tcc 729  
 Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser  
 215 220 225

ctc ggg ccc cag ctc cgc ctc tgc cag gtg tct ggg ctg ttg gcc ctg 777  
 Leu Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu Ala Leu  
 230 235 240

cgg cca ggg tcc tcc ctg cgg atc cgc acc ctc ccc tgg gcc cat ctc 825  
 Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala His Leu  
 245 250 255

aag gct gcc ccc ttc ctc acc tac ttc gga ctc ttc cag gtt cac tga 873  
 Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val His  
 260 265 270

gcggccgcgg atctgttttaa actag 898

<210> 2  
 <211> 273  
 <212> PRT  
 <213> Artificial Sequence

<400> 2  
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 1 5 10 15  
 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met  
 20 25 30

His

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<220>
<221> CDS
<222> (53) .. (442)
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cgg ggc tcg ctg cgc cgg ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg 106  
 Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly Leu Trp  
                   5                                  10                                  15  
  
 ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc acc gcc 154  
 Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly Thr Ala  
           20                                  25                                  30  
  
 ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag tgc atg 202  
 Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys Cys Met  
           35                                  40                                  45                                  50  
  
 gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc ctg ggc 250  
 Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys Leu Gly  
                                   55                                  60                                  65  
  
 tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg ccc atc ctt 298  
 Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu  
                                   70                                  75                                  80  
  
 ggg ggc gct ctg agc ctg acc ttc gtg ctg ggg ctg ctt tct ggc ttt 346  
 Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser Gly Phe  
           85                                  90                                  95  
  
 ttg gtc tgg aga cga tgc cgc agg aga gag aag ttc acc acc ccc ata 394  
 Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile  
           100                                  105                                  110  
  
 gag gag acc ggc gga gag ggc tgc cca gct gtg gcg ctg atc cag tga 442  
 Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile Gln  
           115                                  120                                  125                                  130  
  
 caatgtgccc cctgccagcc ggggctcgcc cactcatcat tcattcatcc attctagagc 502  
 cagtctctgc ctcccagacg cggcggggagc caagctcttc caaccacaag ggggggtgggg 562  
 ggcggtgaat cacctctgag gcttggggccc aggggttcagg ggaaccttcc aagggtgtctg 622  
 gttgccctgc ctctggctcc agaacagaaa gggagcctca cgctgggtca cacaaaacag 682  
 ctgacactga ctaaggaact gcagcatttg cacaggggag ggggggtgccc tccttcctag 742  
 aggccctggg ggccaggctg acttggggggg cagacttgac actaggcccc actcactcag 802  
 atgtcctgaa attccaccac ggggggtcacc ctgggggggtt agggacctat ttttaacact 862  
 agagggg 868

&lt;210&gt; 4

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly  
           1                                  5                                  10                                  15  
  
 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly  
                                   20                                  25                                  30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys  
           35                          40                          45  
 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys  
           50                          55                          60  
 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro  
           65                          70                          75                          80  
 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser  
                           85                          90                          95  
 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr  
                           100                          105                          110  
 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile  
           115                          120                          125

Gln

<210> 5  
 <211> 129  
 <212> PRT  
 <213> Mus sp.

<400> 5  
 Met Ala Pro Gly Trp Pro Arg Ser Leu Pro Gln Ile Leu Val Leu Gly  
           1                          5                          10                          15  
 Phe Gly Leu Val Leu Met Arg Ala Ala Ala Gly Glu Gln Ala Pro Gly  
                           20                          25                          30  
 Thr Ser Pro Cys Ser Ser Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys  
           35                          40                          45  
 Cys Met Asp Cys Ala Ser Cys Pro Ala Arg Pro His Ser Asp Phe Cys  
           50                          55                          60  
 Leu Gly Cys Ala Ala Ala Pro Pro Ala His Phe Arg Leu Leu Trp Pro  
           65                          70                          75                          80  
 Ile Leu Gly Gly Ala Leu Ser Leu Val Leu Val Leu Ala Leu Val Ser  
                           85                          90                          95  
 Ser Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr  
                           100                          105                          110  
 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Gly Val Ala Leu Ile  
           115                          120                          125

Gln

<210> 6  
 <211> 932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS

&lt;222&gt; (1)..(930)

&lt;220&gt;

<223> Description of Artificial Sequence: human TWEAK  
receptor fusion protein construct

&lt;400&gt; 6

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Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly	
1 5 10 15	
ctc tgg ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc	96
Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly	
20 25 30	
acc gcc ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag	144
Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys	
35 40 45	
tgc atg gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc	192
Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys	
50 55 60	
ctg ggc tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg aga	240
Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Arg	
65 70 75 80	
tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc	288
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala	
85 90 95	
gag ggc gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc	336
Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr	
100 105 110	
ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg	384
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val	
115 120 125	
agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg	432
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val	
130 135 140	
gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc	480
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser	
145 150 155 160	
acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg	528
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu	
165 170 175	
aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc	576
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala	
180 185 190	
ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca	624
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro	
195 200 205	
cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag	672
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln	
210 215 220	

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gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc 720
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
225                230                235                240

gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg 768
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
                245                250                255

cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat agc aag ctc 816
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                260                265                270

acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc 864
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                275                280                285

gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc 912
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                290                295                300

ctg tct ccg ggt aaa tga ac 932
Leu Ser Pro Gly Lys
305                310

<210> 7
<211> 309
<212> PRT
<213> Artificial Sequence

<400> 7
Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
 1                5                10                15

Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
                20                25                30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35                40                45

Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
 50                55                60

Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Arg
 65                70                75                80

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
                85                90                95

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 100                105                110

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 115                120                125

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 130                135                140

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 145                150                155                160

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006727 "45424260

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
 165, 170 175  
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
 180 185 190  
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
 195 200 205  
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
 210 215 220  
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 225 230 235 240  
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 245 250 255  
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
 260 265 270  
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
 275 280 285  
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
 290 295 300  
 Leu Ser Pro Gly Lys  
 305

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